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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=5; day=11; hr=17; min=36; sec=25; ms=624;]

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Application No: 10535522 Version No: 3.0

Input Set:

Output Set:

Started: 2009-05-05 16:25:49.936
Finished: 2009-05-05 16:25:51.056
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 120 ms
Total Warnings: 8
Total Errors: 0
No. of SeqIDs Defined: 13
Actual SeqID Count: 13

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SEQUENCE LISTING

<110> Steinkasserer, Alexander

<120> Use of Soluble Forms of CD83 and Nucleic Acids Encoding
them for the Treatment or Prevention of Diseases

<130> 032723woJH

<140> 10535522

<141> 2006-04-13

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 618

<212> DNA

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<220>

<221> CDS

<222> (1)..(615)

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1 5 10 15	

gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac	96
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp	
20 25 30	

ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc	144
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser	
35 40 45	

tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag	192
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln	
50 55 60	

gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt	240
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly	
65 70 75 80	

tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac	288
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn	
85 90 95	

act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg	336
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro	
100 105 110	

gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga	384
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly	

115	120	125	
tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag			432
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu			
130	135	140	
att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att			480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile			
145	150	155	160
ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct			528
Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser			
165	170	175	
aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag			576
Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys			
180	185	190	
cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga			618
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Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser			
35	40	45	
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln			
50	55	60	
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly			
65	70	75	80
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn			
85	90	95	
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro			
100	105	110	
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly			
115	120	125	
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu			
130	135	140	
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile			

145		150		155		160
Phe Thr Cys Lys	Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser					
	165		170		175	
Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys						
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His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val						
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<220>
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 <222> (14)..(601)

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gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct	97
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala	
15 20 25	
tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag	145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln	
30 35 40	
ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag	193
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu	
45 50 55 60	
agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc	241
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro	
65 70 75	
agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc	289
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser	
80 85 90	
tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac	337
Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn	
95 100 105	
ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct	385
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala	
110 115 120	
aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc	433
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe	
125 130 135 140	

tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt	481
Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe	
145 150 155	
gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa	529
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu	
160 165 170	
caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg	577
Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val	
175 180 185	
acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggg ttttaciaag	631
Thr Leu Pro Lys Thr Glu Thr Val	
190 195	
ccaagggcac atcagatcag tgtgctgaa tgccacccgg acaagagaag aatgagctcc	691
atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc	751
cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgcttct	811
ctgtggctgt cagcttaatg tttcatgtgg ctatctgggc aacctcgtga gtgcttttca	871
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tgagctggcc ctgtgacaga ctctgagga cagctgtcct ctctacatc tgggatacat	991
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gacaggccaa gctgtgagcc agtgggaaat atttagcaaa taatttccca gtgcgaaggt	1111
cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagtg aactattccc	1171
cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcca	1231
catttatattt tttaatcttc atgtacttgt caaagaagaa ttttcatgt tttttcaaag	1291
aagtgtgttt ctttcctttt ttaaaatatg aaggtctagt tacatagcat tgctagctga	1351
caagcagcct gagagaagat ggagaatgtt cctcaaaata gggacagcaa gctagaagca	1411
ctgtacagtg cctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac	1471
aagattgtct gtatgattct ggacgagtca cttgtgggtt tcaactctctg gttagtaaac	1531
cagatagttt agtctgggtt gaatacaatg gatgtgaagt tgcttgggga aagctgaatg	1591
tagtgaatac attggcaact ctactgggct gttaccttgt tgatatacta gagttctgga	1651
gctgagcgaa tgctgtcat atctcagctt gcccatcaat ccaaacacag gaggctacaa	1711
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gcgctttgcg cttgaaggac taatcacaag ttcttgaaga tatggaccta ggggagctat 1831
 tgcgccacga caggaggaag ttctcagatg ttgcattgat gtaacattgt tgcatttctt 1891
 taatgagctg ggctccttcc tcatttgctt cccaaagaga ttttgtccca ctaatggtgt 1951
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 Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
 35 40 45
 Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
 50 55 60
 Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
 65 70 75 80
 Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
 85 90 95
 Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
 100 105 110
 Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
 115 120 125
 Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
 130 135 140
 Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
 145 150 155 160
 Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
 165 170 175
 Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
 180 185 190
 Thr Glu Thr Val
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<210> 5
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for CD83ext

 <400> 5
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 <210> 6
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer for CD83ext

 <400> 6
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 <210> 7
 <211> 435
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: partial
 sequence of pGEX2ThCD83ext
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 <222> (1)..(417)
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 gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc 96
 Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
 10 15 20

 tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144
 Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
 25 30 35

 ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192
 Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
 40 45 50 55

 cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
 60 65 70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288
 Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
 75 80 85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336
 Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
 90 95 100

agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa 384
 Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
 105 110 115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435
 Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
 120 125 130

<210> 8
 <211> 139
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: partial
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Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
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Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
 25 30 35

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
 40 45 50 55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
 60 65 70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
 75 80 85

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
 90 95 100

Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
 105 110 115

Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
 120 125 130

<210> 9
<211> 435
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext_mut129_CtoS

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<222> (1)..(417)
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<221> mat_peptide
<222> (28)..(417)

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Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
10 15 20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag 144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
25 30 35

ggg ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga 192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
40 45 50 55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat 240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
60 65 70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg 288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
75 80 85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta 336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
90 95 100

agt ggc aag gtg atc ttg aga gtg aca gga tcc cct gca cag cgt aaa 384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys
105 110 115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120 125 130

<210> 10
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext_mut129_CtoS

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